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SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

THE UNIVERSITY OF TOKYO

<120> METHOD FOR DIAGNOSING HEPATOCELLULAR CARCINOMAS

<130> ONC-A0305P

<150> US 60/505,632

<151> 2003-09-24

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 1528

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133).. (1308)

<223>

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ctcgccctac tgagcgagcg gcccggggcg ccgaggggtc cgcgccgcgc ggggcgcacc 120

gccctggccg cc atg tgc tcc cag ctc tgg ttc ctg acg gac cgg cgc atc 171

Met Cys Ser Gln Leu Trp Phe Leu Thr Asp Arg Arg Ile

1

5

10

cgc gag gac tac ccg cag gtg cag atc ctg cgc gcc ctc cgg cag cgc 219

Arg Glu Asp Tyr Pro Gln Val Gln Ile Leu Arg Ala Leu Arg Gln Arg

15

20

25

tgc tcc gag cag gac gtg cgc ttc cgg gcg gtg ctt atg gac cag atc 267

Cys Ser Glu Gln Asp Val Arg Phe Arg Ala Val Leu Met Asp Gln Ile

30

35

40

45

gcc gtc acc atc gtc ggc ggc cac ctc ggc ctc cag cta aac cag aag 315

Ala Val Thr Ile Val Gly Gly His Leu Gly Leu Gln Leu Asn Gln Lys

50

55

60

gcc ctc acc act ttc ccg gat gtg gtg ctt gta cgg gta ccc aca ccc 363

Ala Leu Thr Thr Phe Pro Asp Val Val Leu Val Arg Val Pro Thr Pro

65

70

75

tca gtg cag tca gac agt gac atc act gtc ctg cga cac ctg gag aag 411

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Ser Val Gln Ser Asp Ser Asp Ile Thr Val Leu Arg His Leu Glu Lys

80

85

90

ctg ggc tgc cgg ttg gtc aat cgc cca cag agc atc tta aat tgc atc 459

Leu Gly Cys Arg Leu Val Asn Arg Pro Gln Ser Ile Leu Asn Cys Ile

95

100

105

aac aaa ttc tgg acg ttc caa gaa ctg gct gga cat ggg gtc ccc atg 507

Asn Lys Phe Trp Thr Phe Gln Glu Leu Ala Gly His Gly Val Pro Met

110

115

120

125

cca gac acc ttc tcc tat ggt ggg cat gaa gac ttt tca aaa atg att 555

Pro Asp Thr Phe Ser Tyr Gly Gly His Glu Asp Phe Ser Lys Met Ile

130

135

140

gat gaa gct gag ccc ctg ggc tac cca gtc gtg gtg aag agc aca cga 603

Asp Glu Ala Glu Pro Leu Gly Tyr Pro Val Val Val Lys Ser Thr Arg

145

150

155

ggc cac cgg gga aaa gct gtt ttt ctg gca aga gat aaa cat cac ctc 651

Gly His Arg Gly Lys Ala Val Phe Leu Ala Arg Asp Lys His His Leu

160

165

170

tct gac atc tgc cat ctg atc cgc cac gat gtg ccc tac ctg ttc cag 699

Ser Asp Ile Cys His Leu Ile Arg His Asp Val Pro Tyr Leu Phe Gln

175

180

185

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aag tac gtg aag gag tcc cat gga aag gac atc cgg gtg gtg gtg gta 747
Lys Tyr Val Lys Glu Ser His Gly Lys Asp Ile Arg Val Val Val Val
190 195 200 205

ggg ggc cag gtc ata ggc tct atg ctt cgc tgc tcc act gat gga cgg 795
Gly Gly Gln Val Ile Gly Ser Met Leu Arg Cys Ser Thr Asp Gly Arg
210 215 220

atg cag agc aac tgc tct ctc ggt ggc gtg ggc gtc aag tgt ccg ctg 843
Met Gln Ser Asn Cys Ser Leu Gly Gly Val Gly Val Lys Cys Pro Leu
225 230 235

aca gaa caa ggc aag cag ttg gct att cag gtg tcc aac atc cta ggc 891
Thr Glu Gln Gly Lys Gln Leu Ala Ile Gln Val Ser Asn Ile Leu Gly
240 245 250

atg gac ttc tgt ggc att gat ctc ctt atc atg gac gat ggc tcc ttt 939
Met Asp Phe Cys Gly Ile Asp Leu Leu Ile Met Asp Asp Gly Ser Phe
255 260 265

gtg gtg tgt gag gca aat gct aat gtt ggc ttc cta gcc ttt gac cag 987
Val Val Cys Glu Ala Asn Ala Asn Val Gly Phe Leu Ala Phe Asp Gln
270 275 280 285

gca tgc aac tta gat gtg ggt ggg atc att gca gac tat acc atg tcc 1035

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Ala Cys Asn Leu Asp Val Gly Gly Ile Ile Ala Asp Tyr Thr Met Ser

290

295

300

ttg ctg cca aat agg cag act gga aag atg gct gtc ctc cca gga ctg 1083

Leu Leu Pro Asn Arg Gln Thr Gly Lys Met Ala Val Leu Pro Gly Leu

305

310

315

tcg agt cca agg gag aag aac gag ccg gat ggc tgt gct tca gct cag 1131

Ser Ser Pro Arg Glu Lys Asn Glu Pro Asp Gly Cys Ala Ser Ala Gln

320

325

330

gga gtt gca gag agc gtc tat acc atc aac agt ggg tct acc tct agc 1179

Gly Val Ala Glu Ser Val Tyr Thr Ile Asn Ser Gly Ser Thr Ser Ser

335

340

345

gaa agt gag cct gaa ctg gga gag atc cgg gat tcc tca gca agc aca 1227

Glu Ser Glu Pro Glu Leu Gly Glu Ile Arg Asp Ser Ser Ala Ser Thr

350

355

360

365

atg ggg gcc cca ccc tcc atg ctg ccc gaa cct ggc tac aac att aac 1275

Met Gly Ala Pro Pro Ser Met Leu Pro Glu Pro Gly Tyr Asn Ile Asn

370

375

380

aac agg att gct tct gag tta aaa ctt aag tga attcctgctt tttaggcagca 1328

Asn Arg Ile Ala Ser Glu Leu Lys Leu Lys

385

390

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tttaaacc aa atcctactgc ttcctagta gttttgagtg aataaaatct ggactaatgt 1388

gatttcattt gcacagaaac tagaaatccc atctgggcac tcagcatttt ttctaacgat 1448

gatttaagca aatggcctag ctttgtggtt ttacaaaga caaatataaa aacactcaca 1508

agaacaaaaa aaaaaaaaaa 1528

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<213> Homo sapiens

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1

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15

Tyr Pro Gln Val Gln Ile Leu Arg Ala Leu Arg Gln Arg Cys Ser Glu

20

25

30

Gln Asp Val Arg Phe Arg Ala Val Leu Met Asp Gln Ile Ala Val Thr

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35

40

45

Ile Val Gly Gly His Leu Gly Leu Gln Leu Asn Gln Lys Ala Leu Thr

50

55

60

Thr Phe Pro Asp Val Val Leu Val Arg Val Pro Thr Pro Ser Val Gln

65

70

75

80

Ser Asp Ser Asp Ile Thr Val Leu Arg His Leu Glu Lys Leu Gly Cys

85

90

95

Arg Leu Val Asn Arg Pro Gln Ser Ile Leu Asn Cys Ile Asn Lys Phe

100

105

110

Trp Thr Phe Gln Glu Leu Ala Gly His Gly Val Pro Met Pro Asp Thr

115

120

125

Phe Ser Tyr Gly Gly His Glu Asp Phe Ser Lys Met Ile Asp Glu Ala

130

135

140

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Glu Pro Leu Gly Tyr Pro Val Val Val Lys Ser Thr Arg Gly His Arg
145 150 155 160

Gly Lys Ala Val Phe Leu Ala Arg Asp Lys His His Leu Ser Asp Ile
165 170 175

Cys His Leu Ile Arg His Asp Val Pro Tyr Leu Phe Gln Lys Tyr Val
180 185 190

Lys Glu Ser His Gly Lys Asp Ile Arg Val Val Val Val Gly Gly Gln
195 200 205

Val Ile Gly Ser Met Leu Arg Cys Ser Thr Asp Gly Arg Met Gln Ser
210 215 220

Asn Cys Ser Leu Gly Gly Val Gly Val Lys Cys Pro Leu Thr Glu Gln
225 230 235 240

Gly Lys Gln Leu Ala Ile Gln Val Ser Asn Ile Leu Gly Met Asp Phe

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245

250

255

Cys Gly Ile Asp Leu Leu Ile Met Asp Asp Gly Ser Phe Val Val Cys

260

265

270

Glu Ala Asn Ala Asn Val Gly Phe Leu Ala Phe Asp Gln Ala Cys Asn

275

280

285

Leu Asp Val Gly Gly Ile Ile Ala Asp Tyr Thr Met Ser Leu Leu Pro

290

295

300

Asn Arg Gln Thr Gly Lys Met Ala Val Leu Pro Gly Leu Ser Ser Pro

305

310

315

320

Arg Glu Lys Asn Glu Pro Asp Gly Cys Ala Ser Ala Gln Gly Val Ala

325

330

335

Glu Ser Val Tyr Thr Ile Asn Ser Gly Ser Thr Ser Ser Glu Ser Glu

340

345

350

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Pro Glu Leu Gly Glu Ile Arg Asp Ser Ser Ala Ser Thr Met Gly Ala

355

360

365

Pro Pro Ser Met Leu Pro Glu Pro Gly Tyr Asn Ile Asn Asn Arg Ile

370

375

380

Ala Ser Glu Leu Lys Leu Lys

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390

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<213> Artificial

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acaacagcct caagatcatc ag

22

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<211> 20

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<400> 4

ggtcaccac tgacacgttg

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caaataggca gactggaaag atg

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<211> 23

<212> DNA

1 2 / 2 7

<213> Artificial

<220>

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<400> 6

ctaggaagc agtaggattt ggt

23

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<213> Artificial

1 3 / 2 7

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aatctcgaga gcaggaattc acttaagttt taactc

36

<210> 9

<211> 22

<212> DNA

<213> Artificial

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tggtagccaa gtgcaggtta ta

22

<210> 10

<211> 22

<212> DNA

<213> Artificial

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1 4 / 2 7

<400> 10

ccaaagggtt tctgcagttt ca

22

<210> 11

<211> 30

<212> DNA

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<400> 11

tgcggatcca gacgagattg tactgagagt

30

<210> 12

<211> 29

<212> DNA

<213> Artificial

<220>

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<400> 12

1 5 / 2 7

ctctatctcg agtgaggcgg aaagaacca

29

<210> 13

<211> 47

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

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tttaagcttg aagaccattt ttggaaaaaa aaaaaaaaaa aaaaaaac

47

<210> 14

<211> 34

<212> DNA

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tttaagcttg aagacatggg aaagagtggc ctca

34

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<210> 15

<211> 51

<212> DNA

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<223> An artificially synthesized oligonucleotide sequence for siRNA

<400> 15

caccgaagca gcacgacttc ttcttcaaga gagaagaagt cgtgctgctt c 51

<210> 16

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for siRNA

<400> 16

aaaagaagca gcacgacttc ttctctcttg aagaagaagt cgtgctgctt c 51

<210> 17

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<211> 51

<212> DNA

<213> Artificial

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<400> 17

tcccggtgcc gctgacagaa caattcaaga gattgttctg tcagcggaca c 51

<210> 18

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for siRNA

<400> 18

aaaagtgtcc gctgacagaa caatctcttg aattgttctg tcagcggaca c 51

<210> 19

<211> 19

<212> DNA

18 / 27

<213> Artificial

<220>

<223> An artificially synthesized target sequence for siRNA

<400> 19

gtgtccgctg acagaacaa

19

<210> 20

<211> 21

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 20

gagtcctga accatctgct c

21

<210> 21

<211> 23

<212> DNA

<213> Artificial

1 9 / 2 7

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 21

caagatgtac agagcatcac agc

23

<210> 22

<211> 29

<212> DNA

<213> Artificial

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<223> An artificially synthesized primer sequence for RT-PCR

<400> 22

attgaattcg catggcgcca cccgcggcg

29

<210> 23

<211> 32

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

20 / 27

<400> 23

aatggtacct caccaaggcc tccagacact cc

32

<210> 24

<211> 51

<212> DNA

<213> Artificial

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<223> An artificially synthesized oligonucleotide sequence for siRNA

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tcccactttt aggaccctg cagttcaaga gactgcaggg tccctaaaag t

51

<210> 25

<211> 51

<212> DNA

<213> Artificial

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2 1 / 2 7

aaaaactttt aggaccctg cagtctcttg aactgcaggg tccctaaaag t 51

<210> 26

<211> 19

<212> DNA

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<400> 26

acttttaggg accctgcag 19

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<213> Homo sapiens

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<222> (125).. (799)

<223>

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22 / 27

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ccgggtcccg cgcgtcccg tccccgtgc tcctagcccc tgccgcgtcc ccggcggagc 120

gggc atg gcg cca ccc gcg gcg cct ggc cgg gac cgt gtg ggc cgt gag 169

Met Ala Pro Pro Ala Ala Pro Gly Arg Asp Arg Val Gly Arg Glu

1 5 10 15

gat gag gac ggc tgg gag acg cga ggg gac cgc aag gcc cgg aag ccc 217

Asp Glu Asp Gly Trp Glu Thr Arg Gly Asp Arg Lys Ala Arg Lys Pro

20 25 30

ctg gtg gag aag aag cgg cgc gcg cgg atc aac gag agc ctg cag gag 265

Leu Val Glu Lys Lys Arg Arg Ala Arg Ile Asn Glu Ser Leu Gln Glu

35 40 45

ctg cgg ctg ctg ctg gcg ggc gcc gag gtg cag gcc aag ctg gag aac 313

Leu Arg Leu Leu Leu Ala Gly Ala Glu Val Gln Ala Lys Leu Glu Asn

50 55 60

gcc gaa gtg ctg gag ctg acg gtg cgg cgg gtc cag ggt gtg ctg cgg 361

Ala Glu Val Leu Glu Leu Thr Val Arg Arg Val Gln Gly Val Leu Arg

65 70 75

ggc cgg gcg cgc gag cgc gag cag ctg cag gcg gaa gcg agc gag cgc 409

Gly Arg Ala Arg Glu Arg Glu Gln Leu Gln Ala Glu Ala Ser Glu Arg

2 3 / 2 7

80	85	90	95	
ttc gct gcc ggc tac atc cag tgc atg cac gag gtg cac acg ttc gtg Phe Ala Ala Gly Tyr Ile Gln Cys Met His Glu Val His Thr Phe Val				457
	100	105	110	
tcc acg tgc cag gcc atc gac gct acc gtc gct gcc gag ctc ctg aac Ser Thr Cys Gln Ala Ile Asp Ala Thr Val Ala Ala Glu Leu Leu Asn				505
	115	120	125	
cat ctg ctc gag tcc atg ccg ctg cgt gag ggc agc agc ttc cag gat His Leu Leu Glu Ser Met Pro Leu Arg Glu Gly Ser Ser Phe Gln Asp				553
	130	135	140	
ctg ctg ggg gac gcc ctg gcg ggg cca cct aga gcc cct gga cgg agt Leu Leu Gly Asp Ala Leu Ala Gly Pro Pro Arg Ala Pro Gly Arg Ser				601
	145	150	155	
ggc tgg cct gcg ggg ggc gct ccg gga tcc cca ata ccc agc ccc ccg Gly Trp Pro Ala Gly Gly Ala Pro Gly Ser Pro Ile Pro Ser Pro Pro				649
160	165	170	175	
ggt cct ggg gac gac ctg tgc tcc gac ctg gag gag gcc cct gag gct Gly Pro Gly Asp Asp Leu Cys Ser Asp Leu Glu Glu Ala Pro Glu Ala				697
	180	185	190	

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gaa ctg agt cag gct cct gct gag ggg ccc gac ttg gtg ccc gca gcc 745

Glu Leu Ser Gln Ala Pro Ala Glu Gly Pro Asp Leu Val Pro Ala Ala

195

200

205

ctg ggc agc ctg acc aca gcc caa att gcc cgg agt gtc tgg agg cct 793

Leu Gly Ser Leu Thr Thr Ala Gln Ile Ala Arg Ser Val Trp Arg Pro

210

215

220

tgg tga ccaatgccag ccagagtcct gcgggggtgg gcccgccct ccctggatct 849

Trp

ctccctcct cccaggggtt cagatgtggt ggggtagggc cctggaagtc tcccaggtct 909

tccctccctc ctctgatgga tggcttcag ggcagccct ggtaaccagc ccagtcaggc 969

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gggagctacg ggcaggagga agaatttgt agagctgcca gcgctctccc aggttcaccc 1089

accagcctt caccagccct gtgcgggctc tgggggcaga ggtggcagga atggtgctgg 1149

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gagatgagag gcagggtcac tcagctgcac tgcccagagc tgtgatgctc tgtacatctt 1269

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gtttgtagca cacttgagtt tgtgtattcc attgacatca aatgtgacaa ttttactaaa 1329

taaagaattt tggagttagt tacccttgaa aaaaaaaaaa aaaaaa 1375

<210> 28

<211> 224

<212> PRT

<213> Homo sapiens

<400> 28

Met Ala Pro Pro Ala Ala Pro Gly Arg Asp Arg Val Gly Arg Glu Asp

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Glu Asp Gly Trp Glu Thr Arg Gly Asp Arg Lys Ala Arg Lys Pro Leu

20 25 30

Val Glu Lys Lys Arg Arg Ala Arg Ile Asn Glu Ser Leu Gln Glu Leu

35 40 45

Arg Leu Leu Leu Ala Gly Ala Glu Val Gln Ala Lys Leu Glu Asn Ala

50 55 60

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Glu Val Leu Glu Leu Thr Val Arg Arg Val Gln Gly Val Leu Arg Gly
65 70 75 80

Arg Ala Arg Glu Arg Glu Gln Leu Gln Ala Glu Ala Ser Glu Arg Phe
 85 90 95

Ala Ala Gly Tyr Ile Gln Cys Met His Glu Val His Thr Phe Val Ser
 100 105 110

Thr Cys Gln Ala Ile Asp Ala Thr Val Ala Ala Glu Leu Leu Asn His
 115 120 125

Leu Leu Glu Ser Met Pro Leu Arg Glu Gly Ser Ser Phe Gln Asp Leu
 130 135 140

Leu Gly Asp Ala Leu Ala Gly Pro Pro Arg Ala Pro Gly Arg Ser Gly
145 150 155 160

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Trp Pro Ala Gly Gly Ala Pro Gly Ser Pro Ile Pro Ser Pro Pro Gly

165

170

175

Pro Gly Asp Asp Leu Cys Ser Asp Leu Glu Glu Ala Pro Glu Ala Glu

180

185

190

Leu Ser Gln Ala Pro Ala Glu Gly Pro Asp Leu Val Pro Ala Ala Leu

195

200

205

Gly Ser Leu Thr Thr Ala Gln Ile Ala Arg Ser Val Trp Arg Pro Trp

210

215

220